SEQUENCE LISTING

<110> BASLER, Konrad

<220> <221>

<222> <223> exon

(4679)..(4870)

```
BRUNNER, Erich
     FROESCH, Barbara
     KRAMPS, Thomas
     PETER, Oliver
<120> ESSENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING PATHWAY AND THERAPEUTIC
AND DIAGNOSTIC APPLICATIONS BASED THEREON
<130> Q60361
<140> 09/915,543
<141> 2001-07-27
<150> 60/221,502
<151> 2000-07-28
<160> 22
<170> PatentIn version 3.1
<210> 1
<211> 6909
<212> DNA
<213> Drosophila lgs
<220>
<221> exon
<222> (691)..(981)
<223>
<220>
<221> exon
<222> (468)..(632)
<223>
<220>
<221>
       exon
<222>
       (1456)..(1665)
<223>
<220>
<221>
       exon
       (2394)..(4397)
<222>
<223>
```

<220> <221> exon <222> (4927) . . (6456) <223> <400> 1 acgagtgctt ctcttattat gcgagctgtt tattccaaag tatgttcgca attttcgact 60 120 cctgctaaca taacgcacgg ttaaagcagg aacatttggg cctataagcc caaaatttca ttagcttaat acgatgctcc gaagtgttat tgcatttgca catatacata aaattgtgac 180 atagaatagg agaattccac atacaaatac aaaaatacaa aatcctccag taaaatttaa 240 300 aacgatatcg tgttttgctt cgcgtatctc acgtgagatg taatcgcatg catatgagtg gtgagtgcct gcgtgcagtt cctggtctaa atatgcttaa ttgcgttcgc cgacttcaaa 360 agcaataaaa cgatggattt taattgctac ttgagcaatt agccacacaa gggatcttgg 420 gaaggtcgat ttgaaggaat tcgatttcta ggatgctctc gacaaca atg ccc cgc 476 Met Pro Arg 1 524 agt cca acc caa caa cag ccg caa cca aac tcc gat gcc tcc tca aca Ser Pro Thr Gln Gln Pro Gln Pro Asn Ser Asp Ala Ser Ser Thr 5 10 15 agt gca tct gga tca aat cct gga gca gcg atc gga aat ggg gac tcg 572 Ser Ala Ser Gly Ser Asn Pro Gly Ala Ala Ile Gly Asn Gly Asp Ser 20 25 30 35 gcg gcg agc aga agt tct ccg aag acc ctt aat agc gaa ccc ttt tct 620 Ala Ala Ser Arg Ser Ser Pro Lys Thr Leu Asn Ser Glu Pro Phe Ser 40 45 50 672 act ttg tcg ccg ggtaagactt gtattgattt ctctttgtcc ggaattataa Thr Leu Ser Pro 55 caactttctg tgtttcca gat caa ata aaa ttg acg cca gaa gaa ggc act 723 Asp Gln Ile Lys Leu Thr Pro Glu Glu Gly Thr gag aaa agc gga cta tca act agt gat aaa gct gcc act gga gga gcc 771 Glu Lys Ser Gly Leu Ser Thr Ser Asp Lys Ala Ala Thr Gly Gly Ala 70 75 80 cca ggc agt gga aat aat ctg ccc gag gga caa act atg cta agg cag 819 Pro Gly Ser Gly Asn Asn Leu Pro Glu Gly Gln Thr Met Leu Arg Gln 85 90 95

aac tot acg ago aca atc aac tog tgo cta gto got tot cca caa aac

Asn Ser Thr Ser Thr Ile Asn Ser Cys Leu Val Ala Ser Pro Gln Asn

110

105

100

tcc agt gaa cac tcg aat agc agc aat gtg tct gct aca gtg ggc ctt Ser Ser Glu His Ser Asn Ser Ser Asn Val Ser Ala Thr Val Gly Leu 115 120 125 130	915
act cag atg gta gat tgt gac gag caa tcg aag aaa aac aaa tgt agt Thr Gln Met Val Asp Cys Asp Glu Gln Ser Lys Lys Asn Lys Cys Ser 135 140 145	963
gtg aag gac gag gaa gct ggtaagactg ccctacaaat ggtttaaaat Val Lys Asp Glu Glu Ala 150	1011
tttaaaatgt attggcgttc acctttgtta atcatttaat tgtttttttt ttgctatact	1071
tacaatttta gttttaaact tgtaaacttg actaaaactc gcgaagctcg gatcaaaaca	1131
gacattttct tggaaccgta attaagctca taaaaatatt aattcatctt gatggaatgc	1191
atatcataga tgtactcaaa catctcaaga aagacctcaa attggatcaa ctaattagtt	1251
tgagaaaaaa ttgctgtact tttaagaata tattaattta aaaatttgct gagtgaaatg	1311
atataatagt cacaataatt tttagttaaa ctgctaaagc attttgaata gccgtgctac	1371
gcagatgcta ctagacgcgg tgtaaaagct aatttttatt taaaagctgt cctaatattc	1431
cataaccatt aatgtcccat ttca gaa ata agt tct aat aaa gca aaa ggt Glu Ile Ser Ser Asn Lys Ala Lys Gly 155 160	1482
caa gca gct ggt ggc ggc tgc gaa aca ggt tct aca tcc agt ttg act Gln Ala Ala Gly Gly Cys Glu Thr Gly Ser Thr Ser Ser Leu Thr 165 170 175	1530
gtc aag gaa gaa ccc acc gat gtc tta ggc agt tta gta aat atg aaa Val Lys Glu Glu Pro Thr Asp Val Leu Gly Ser Leu Val Asn Met Lys 180 185 190	1578
aaa gaa gaa aga gaa aat cat tcg cca acg atg tcc cct gtt ggt ttt Lys Glu Glu Arg Glu Asn His Ser Pro Thr Met Ser Pro Val Gly Phe 195 200 205	1626
ggt tca att ggt aat gca cag gac aac tcc gct aca ccg ggtaagtttt Gly Ser Ile Gly Asn Ala Gln Asp Asn Ser Ala Thr Pro	1675
210 215 220	
aagagatcca tataaagcaa ataacaagaa ttaatgtcag ttaccaattt tatttgatag	1735
	1735 1795
aagagatcca tataaagcaa ataacaagaa ttaatgtcag ttaccaattt tatttgatag	
aagagatcca tataaagcaa ataacaagaa ttaatgtcag ttaccaattt tatttgatag tcaaagaact actatagcga tatctcctgc cttttaattt tattttaatt aggaaatacg	1795

ggaaaatggg tgtaatt	tttg taggaagtt	t tcattttaga	agaaatgtga ttattttatt	2035
aaaccccttc aagcgga	aact acatttgtt	c tacgatattt	tggaaaaaca aatggttaag	2095
ttggaaagtg cctataa	aaac agaattcca	c ggtttcaaat	actaaccagg tttttgattt	2155
aattttgatt aaatgag	gaaa ttatcacac	t tcagttaaaa	tgtttaattc gattaaggtc	2215
ggacaatcac agcaga	tttc catttttgc	g tgtatatata	gaagtcgcct tcacactctt	2275
ctggcgcgct tcaccad	ctac gtggagtto	c gcccgcagtg	atttatatag atgatttacg	2335
agttatttaa tttttt	atgg tgtatttta	a taaatatctt	atttattcat tttacata	2393
		Asp Ser Thr	acg gaa aaa aaa gga Thr Glu Lys Lys Gly 235	2441
			atg gaa ggc tgc aat Met Glu Gly Cys Asn 250	2489
		_	aat aat cct gca att Asn Asn Pro Ala Ile 270	2537
Ser Ser Ile Leu V			ccc gga atc gga gtt Pro Gly Ile Gly Val 285	2585
		-	gcc aat gga atc tcc Ala Asn Gly Ile Ser 300	2633
		o Tyr Met Gln	cag caa aat cac ata Gln Gln Asn His Ile 315	2681
			gcc gaa tca gtt tta Ala Glu Ser Val Leu 330	2729
			tgc act cag cct gct Cys Thr Gln Pro Ala 350	2777
Thr Lys Ser Phe L		_	aac cct tta aag att Asn Pro Leu Lys Ile 365	2825
			cca tgg ata ggc atg Pro Trp Ile Gly Met 380	2873
		o Asn Pro Val	gcc aaa ata aca caa Ala Lys Ile Thr Gln 395	2921

-

cag Gln	_															2969
caa Gln 415		_		_		_	_		_	_			_			3017
	_	_	_		_		_		aac Asn 440	_		_	_	_		3065
	_							-	agg Arg							3113
		_	_	_		_			agc Ser	-		_	_			3161
Ile	_	Glu	Ala	Ala	Gly	Val	Asp	Leu	gga Gly	Gln	Val	Thr		_		3209
_			_			_			att Ile	_		_				3257
	_								caa Gln 520				_			3305
_	_	_	_					_	aat Asn						_	3353
	_			_		_		_	agc Ser		_					3401
				_			_	_	ggt Gly							3449
		_	_	_	_		_		atg Met		Gly		_		tcg Ser 590	3497
			_		_	_			ctt Leu 600	_	—	_	_		_	3545
		_	_	Ile		_	_			_				Asn	aat Asn	3593

aat Asn	caa Gln	aaa Lys 625	acc Thr	agt Ser	gtg Val	caa Gln	tgt Cys 630	gga Gly	tct Ser	gga Gly	gta Val	ggt Gly 635	gtt Val	gtc Val	act Thr	3641
gga Gly	aca Thr 640	act Thr	gca Ala	gct Ala	gga Gly	gta Val 645	aat Asn	gtc Val	aat Asn	atg Met	cat His 650	tgc Cys	tca Ser	agc Ser	tcc Ser	3689
ggc Gly 655	gcc Ala	ccg Pro	aat Asn	ggc Gly	aat Asn 660	atg Met	atg Met	gga Gly	agc Ser	tct Ser 665	acg Thr	gat Asp	atg Met	cta Leu	gcc Ala 670	3737
tcg Ser	ttt Phe	ggc Gly	aac Asn	aca Thr 675	agc Ser	tgc Cys	aac Asn	gtc Val	atc Ile 680	gga Gly	acg Thr	gcc Ala	cca Pro	gat Asp 685	atg Met	3785
tct Ser	aag Lys	gaa Glu	gtt Val 690	tta Leu	aat Asn	caa Gln	gat Asp	agc Ser 695	cga Arg	acc Thr	cat His	tca Ser	cat His 700	caa Gln	ggg Gly	3833
gga Gly	gtt Val	gct Ala 705	caa Gln	atg Met	gag Glu	tgg Trp	tcg Ser 710	aag Lys	att Ile	caa Gln	cat His	caa Gln 715	ttt Phe	ttc Phe	gaa Glu	3881
Glu	Arg 720	Leu	Lys	Gly	Gly	Lys 725	Pro	Arg	Gln	Val	Thr 730	Gly	Thr	Val		3929
cca Pro 735	caa Gln	cag Gln	caa Gln	acc Thr	cct Pro 740	tct Ser	gga Gly	tct Ser	ggt Gly	gga Gly 745	aac Asn	tcg Ser	tta Leu	aac Asn	aac Asn 750	3977
cag Gln	gtg Val	cga Arg	ccc Pro	ctg Leu 755	caa Gln	ggt Gly	cca Pro	cct Pro	cct Pro 760	cct Pro	tac Tyr	cac His	tcc Ser	atc Ile 765	cag Gln	4025
aga Arg	tct Ser	gcg Ala	tca Ser 770	gta Val	cca Pro	ata Ile	gcc Ala	act Thr 775	caa Gln	tcg Ser	ccc Pro	aat Asn	ccc Pro 780	tcg Ser	agt Ser	4073
Pro	Asn	Asn 785	Leu	Ser	Leu	Pro	Ser 790	Pro	Arg	Thr	Thr	Ala 795	Ala	Val		4121
Gly	Leu 800	ccg Pro	Thr	Asn	Ser	Pro 805	Ser	Met	Asp	Gly	Thr 810	Gly	Ser	Leu	Ser	4169
Gly 815	Ser	gtt Val	Pro	Gln	Ala 820	Asn	Thr	Ser	Thr	Val 825	Gln	Ala	Gly	Thr	Thr 830	421.7
aca Thr	gtg Val	ctc Leu	tca Ser	gca Ala 835	aac Asn	aag Lys	aac Asn	tgt Cys	ttt Phe 840	cag Gln	gca Ala	gac Asp	acc Thr	cca Pro 845	tcg Ser	4265
ccg	tca	aat	caa	aat	cgt	agt	aga	aat	acc	gga	tcg	tca	agc	gtt	ctt	4313

Pro Ser Asn Gln Asn Arg Ser Arg Asn Thr Gly Ser Ser Ser Val Leu 850 855 860	
acg cat aac tta agc agc aac cca agt acc ccc tta tct cat cta tcc Thr His Asn Leu Ser Ser Asn Pro Ser Thr Pro Leu Ser His Leu Ser 865 870 875	4361
cca aag gaa ttt gag tct ttc ggt cag tcc tct gct ggtatgttat Pro Lys Glu Phe Glu Ser Phe Gly Gln Ser Ser Ala 880 885 890	4407
atttgtttaa tttttttaaa gacaaatcaa atatgaattg cgttaataat aagttatata	4467
ttacataact cggaaatttg atagaaaaaa tcaggaatag aaaaaataaa ttattttccg	4527
gaccgcccat ccatttcttg aatccaattt ctggagtgat tgttagagat aatctactat	4587
taaaattaaa cacgaaaatt catatccgtt aattgaaaat cactattgtt taataagaaa	4647
ttaaaaatat gtttattata atatttctac a ggt gat aac atg aaa agt agg Gly Asp Asn Met Lys Ser Arg 895	4699
cga cca agc cca cag ggt cag cgg tca cca gta aat agt cta ata gag Arg Pro Ser Pro Gln Gly Gln Arg Ser Pro Val Asn Ser Leu Ile Glu 900 905 910	4747
gca aat aaa gat gta cga ttt gct gca tcc agt cct ggt ttt aac ccg Ala Asn Lys Asp Val Arg Phe Ala Ala Ser Ser Pro Gly Phe Asn Pro 915 920 925	4795
cat cca cat atg caa agc aat tca aat tca gca tta aac gcc tat aaa His Pro His Met Gln Ser Asn Ser Asn Ser Ala Leu Asn Ala Tyr Lys 930 935 940 945	4843
atg ggc tct acc aat ata cag atg gag gtaaatattt aaatatttta Met Gly Ser Thr Asn Ile Gln Met Glu 950	4890
tttaacgttt ttgtgttaat ttatcttctt tttcag cgt caa gca tca gcg caa Arg Gln Ala Ser Ala Gln 955 960	4944
ggt gga tcc gta caa ttt agt cgg cgc tcc gat aat att ccg cta aat Gly Gly Ser Val Gln Phe Ser Arg Arg Ser Asp Asn Ile Pro Leu Asn 965 970 975	4992
ccc aat agt ggc aat cgg ccg cca cca aac aag atg acc caa aac ttc Pro Asn Ser Gly Asn Arg Pro Pro Pro Asn Lys Met Thr Gln Asn Phe 980 985 990	5040
gat cca atc tct tct ttg gca caa atg tcc caa caa cta aca agt tgc Asp Pro Ile Ser Ser Leu Ala Gln Met Ser Gln Gln Leu Thr Ser Cys 995 1000 1005	5088
gtg tcc agc atg ggt agt cca gcc gga act ggt ggt atg acg atg	

1010 1015 1020

atg Met	999 Gly 1025	ggt Gly	ccg Pro	gga Gly	ccg Pro	tcc Ser 1030	Asp	atc Ile	aat Asn	att Ile	gag Glu 1035	cat His	gga Gly	ata Ile	5178
att Ile	tcg Ser 1040	Gly	cta Leu	gat Asp	gga Gly	tca Ser 1045	gga Gly	ata Ile	gat Asp	acc Thr	ata Ile 1050	aat Asn	caa Gln	aat Asn	5223
aac Asn	tgt Cys 1055	cat His	tca Ser	atg Met	aat Asn	gtc Val 1060	gta Val	atg Met	aac Asn	tca Ser	atg Met 1065	ggt Gly	ccc Pro	cga Arg	5268
atg Met	ctg Leu 1070	aat Asn	cct Pro	aaa Lys	atg Met	tgc Cys 1075	gta Val	gca Ala	ggc Gly	ggt Gly	cca Pro 1080	aat Asn	gga Gly	ccg Pro	5313
cct Pro	ggc Gly 1085	ttt Phe	aat Asn	cct Pro	aat Asn	tcc Ser 1090	ccc Pro	aat Asn	ggt Gly	gga Gly	tta Leu 1095	aga Arg	gag Glu	aat Asn	5358
tcc Ser	ata Ile 1100	gly ggg	tct Ser	ggc Gly	tgt Cys	ggc Gly 1105	tca Ser	gca Ala	aac Asn	tct Ser	tca Ser 1110	aac Asn	ttt Phe	caa Gln	5403
Gly 999	gtt Val 1115	Val	cca Pro	cct Pro	ggt Gly	gcc Ala 1120	aga Arg	atg Met	atg Met	ggt Gly	cga Arg 1125	atg Met	cca Pro	gtc Val	5448
Asn	Phe 1130	Gly	Ser	Asn	Phe	aat Asn 1135	Pro	Asn	Ile	Gln	Val 1140	Lys	Ala	Ser	5493
Thr	Pro 1145	Asn	Thr	Ile	Gln	tac Tyr 1150	Met	Pro	Val	Arg	Ala 1155	Gln	Asn	Ala	5538
	aac Asn 1160	aat Asn	aac Asn	aac Asn	aat Asn	gga Gly 1165	gct Ala	aat Asn	aat Asn	gtg Val	cga Arg 1170	atg Met	cca Pro	cct Pro	5583
a gt Ser	ctg Leu 1175	gaa Glu	ttt Phe	ttg Leu	cag Gln	agg Arg 1180	tac Tyr	gct Ala	aac Asn	cct Pro	caa Gln 1185	atg Met	ggt Gly	gct Ala	5628
gta Val	aac	aat	aaa	tca	CCa	ata	tgc	cca	cca	tca	gcc	agc	gac	aat	5673
	Gly 1190	Asn	Gly	Ser	Pro	Ile 1195	Cys	Pro	Pro	Ser	Ala 1200	Ser	Asp	Gly	
act Thr	Gly 1190 cct	Asn	Gly	Ser	Pro gga	Ile	Cys	Pro	gga	Ser	1200 gga	Ser	Asp	Gly	5718

						aat Asn 1240	Gly								5808
aat Asn	caa Gln 1250	atg Met	tct Ser	att Ile	gtt Val	gac Asp 1255	gaa Glu	gag Glu	ggt Gly	gga Gly	tta Leu 1260	ccc Pro	ggc Gly	cat His	5853
gac Asp	gga Gly 1265	tca Ser	atg Met	aat Asn	att Ile	ggt Gly 1270	caa Gln	cca Pro	tct Ser	atg Met	ata Ile 1275	agg Arg	ggc Gly	atg Met	5898
cgt Arg	cca Pro 1280	cat His	gcc Ala	atg Met	cgg Arg	cca Pro 1285	aat Asn	gta Val	atg Met	ggt Gly	gcg Ala 1290	cgg Arg	atg Met	cca Pro	5943
ccc Pro	gtt Val 1295	aac Asn	agg Arg	caa Gln	att Ile	cag Gln 1300	ttt Phe	gca Ala	cag Gln	tca Ser	tcg Ser 1305	gat Asp	ggt Gly	att Ile	5988
gac Asp	tgt Cys 1310	gtc Val	ggg Gly	gat Asp	ccg Pro	tca Ser 1315	tca Ser	ttt Phe	ttc Phe	act Thr	aac Asn 1320	gct Ala	tcc Ser	tgc Cys	6033
aac Asn	agc Ser 1325	gct Ala	gga Gly	cca Pro	cac His	atg Met 1330	ttt Phe	gga Gly	tca Ser	gca Ala	caa Gln 1335	cag Gln	gcc Ala	aat Asn	6078
cag Gln	cct Pro 1340	aag Lys	aca Thr	caa Gln	cac His	ata Ile 1345	Lys	aac Asn	ata Ile	cct Pro	agt Ser 1350	gga Gly	atg Met	tgt Cys	6123
caa Gln	aac Asn 1355	caa Gln	tcg Ser	gga Gly	ctt Leu	gca Ala 1360	gtg Val	gca Ala	caa Gln	Gly	cag Gln 1365	atc Ile	caa Gln	ctg Leu	6168
cat His	999 Gly 1370	caa Gln	gga Gly	cat His	gcg Ala	cag Gln 1375	ggt Gly	cag Gln	tct Ser	tta Leu	att Ile 1380	gga Gly	cct Pro	act Thr	6213
aat Asn	aat Asn 1385	aat Asn	tta Leu	atg Met	tca Ser	act Thr 1390	gcc Ala	gga Gly	agt Ser	gtc Val	agt Ser 1395	gct Ala	act Thr	aac Asn	6258
ggt Gly	gtc Val 1400	tct Ser	ggc Gly	atc Ile	aat Asn	ttc Phe 1405	Val	Gly	Pro	Ser	tct Ser 1410	Thr	Asp	Leu	6303
aag Lys	tat Tyr 1415	gcc Ala	cag Gln	caa Gln	tat Tyr	cat His 1420	agt Ser	ttt Phe	cag Gln	cag Gln	cag Gln 1425	tta Leu	tat Tyr	gct Ala	6348
acc Thr	aac Asn 1430	acc Thr	aga Arg	agt Ser	caa Gln	caa Gln 1435	caa Gln	cag Gln	cat His	atg Met	cac His 1440	cag Gln	cag Gln	cac His	6393

```
cag age aac atg ata aca atg ccg ccg aat tta tca cca aat cca
                                                                    6438
Gln Ser Asn Met Ile Thr Met Pro Pro Asn Leu Ser Pro Asn Pro
    1445
                         1450
                                              1455
acg ttc ttt gtc aac aaa taaacttcta aatttttgcc gccctcgtca
                                                                    6486
        Phe Val Asn Lys
Thr Phe
    1460
tgtattgttt actagtctcc aaattaagac atgcatctct aaataagatt ttttgaagct
                                                                    6546
tatttactta ggtgttttta caacggagaa aataaacttt tggatatgca aatgataacg
                                                                    6606
ttggaaacaa cataattcat ttgcaacttt tagaagtcac gtcgaagtta aatgtagaat
                                                                    6666
ctgtatttta acataatagg tcatctgtaa aaataattaa acatcgaaat tttagttatc
                                                                    6726
agcagctatt ttctgttatt atttaatatg tgcgctgctc tctctgtgtt aaatgaaatt
                                                                    6786
aaaatatata tataaatgta aaacgctatt gatatatatt gctctcaact gtattgtaat
                                                                    6846
caatattaag agaactgtaa attcttccat ataaaggtaa tgaaaaaaaa aaaaaaaaa
                                                                    6906
aaa
                                                                    6909
<210> 2
<211> 28
<212> PRT
<213> Drosophila lgs
<400> 2
Ile Phe Val Phe Ser Thr Gln Leu Ala Asn Lys Gly Ala Glu Ser Val
1
                5
                                    10
                                                        15
Leu Ser Gly Gln Phe Gln Thr Ile Ile Ala Tyr His
            20
                                25
<210> 3
<211> 28
<212> PRT
<213> Human lgs/bcl9
<400> 3
Val Tyr Val Phe Ser Thr Glu Met Ala Asn Lys Ala Ala Glu Ala Val
1
                                    10
                                                        15
Leu Lys Gly Gln Val Glu Thr Ile Val Ser Phe His
```

25

20

<210> 4
<211> 35

```
<212> PRT
       Drosophila lgs
<213>
<400> 4
Glu Asn Leu Thr Pro Gln Gln Arg Gln His Arg Glu Glu Gln Leu Ala
                                    10
                                                        15
Lys Ile Lys Lys Met Asn Gln Phe Leu Phe Pro Glu Asn Glu Asn Ser
            20
                                25
                                                    30
Val Gly Ala
        35
<210>
       5
<211>
       35
<212>
      PRT
      Human lgs/bcl9
<213>
<400> 5
Asp Gly Leu Ser Gln Glu Gln Leu Glu His Arg Glu Arg Ser Leu Gln
                5
                                    10
                                                        15
Thr Leu Arg Asp Ile Gln Arg Met Leu Phe Pro Asp Glu Lys Glu Phe
            20
                                25
                                                    30
Thr Gly Ala
        35
<210>
       6
<211> 15
<212>
      PRT
<213>
      Drosophila lgs
<400> 6
Gln Met Glu Trp Ser Lys Ile Gln His Gln Phe Phe Glu Glu Arg
1
                                    10
                                                        15
<210>
      7
<211> 15
<212>
       PRT
<213>
      Human lgs/bcl9
<400> 7
Gln Ile Ala Trp Leu Lys Leu Gln Glu Phe Tyr Glu Glu Lys
                                    10
                                                        15
```

```
<210> 8
<211> 9
<212> PRT
      Drosophila lgs
<213>
<400> 8
Leu Gln Gly Pro Pro Pro Pro Tyr His
1
<210> 9
<211>
<212> PRT
<213>
      Human lgs/bcl9
<400> 9
Val Arg Gly Pro Pro Pro Pro Tyr Gln
1
<210> 10
<211>
      112
      PRT
<212>
<213> Drosophila lgs
<400> 10
Ser Ala Ser Val Pro Ile Ala Thr Gln Ser Pro Asn Pro Ser Ser Pro
1
                5
                                    10
                                                        15
Asn Asn Leu Ser Leu Pro Ser Pro Arg Thr Thr Ala Ala Val Met Gly
            20
                                25
                                                    30
Leu Pro Thr Asn Ser Pro Ser Met Asp Gly Thr Gly Ser Leu Ser Gly
        35
                            40
                                                 45
Ser Val Pro Gln Ala Asn Thr Ser Thr Val Gln Ala Gly Thr Thr
    50
                        55
Val Leu Ser Ala Asn Lys Asn Cys Phe Gln Ala Asp Thr Pro Ser Pro
65
                    70
                                                             80
Ser Asn Gln Asn Arg Ser Arg Asn Thr Gly Ser Ser Ser Val Leu Thr
                85
                                    90
                                                        95
His Asn Leu Ser Ser Asn Pro Ser Thr Pro Leu Ser His Leu Ser Pro
            100
                                105
                                                     110
```

```
<211>
       111
<212>
       PRT
      Human lgs/bcl9
<213>
<400> 11
Gly Pro Pro Pro Thr Ala Ser Gln Pro Ala Ser Val Asn Ile Pro
1
                5
                                     10
                                                         15
Gly Ser Leu Pro Ser Ser Thr Pro Tyr Thr Met Pro Pro Glu Pro Thr
            20
                                 25
                                                     30
Leu Ser Gln Asn Pro Leu Ser Ile Met Met Ser Arg Met Ser Lys Phe
        35
                             40
Ala Met Pro Ser Ser Thr Pro Leu Tyr His Asp Ala Ile Lys Thr Val
    50
                        55
                                             60
Ala Ser Ser Asp Asp Ser Pro Pro Ala Arg Ser Pro Asn Leu Pro
65
                    70
                                         75
                                                             80
Ser Met Asn Asn Met Pro Gly Met Gly Ile Asn Thr Gln Asn Pro Arg
                85
                                     90
                                                         95
Ile Ser Gly Pro Asn Pro Val Val Pro Met Pro Thr Leu Ser Pro
            100
                                 105
                                                     110
<210>
       12
<211>
       16
<212>
       PRT
<213>
      Drosophila lgs
<400> 12
Asn Pro Lys Met Cys Val Ala Gly Gly Pro Asn Gly Pro Pro Gly Phe
1
                                     10
                                                         15
<210>
       13
<211>
       16
<212>
       PRT
<213>
      Human lgs/bcl9
<400>
      13
Asp Ala Ala Leu Cys Lys Pro Gly Gly Pro Gly Gly Pro Asp Ser Phe
                                     10
                                                         15
```

<210>

<210> 14 <211> 4281 <212> DNA <213> Human lgs/bcl9

<400> 14

atgcattcca gtaaccctaa agtgaggagc tctccatcag gaaacacaca gagtagccct 60 aagtcaaagc aggaggtgat ggtccgtccc cctacagtga tgtccccatc tggaaacccc 120 cagctggatt ccaaattctc caatcagggt aaacaggggg gctcagccag ccaatcccag 180 ccatccccct gtgactccaa gagtggggc cataccccta aagcactccc tggcccaggt 240 gggagcatgg ggctgaagaa tggggctgga aatggtgcca agggcaaggg gaaaagggag 300 cgaagtattt ccgccgactc ctttgatcag agagatcctg ggactccaaa cgatgactct 360 gacattaaag aatgtaattc tgctgaccac ataaagtccc aggattccca gcacacacca 420 cactcgatga ccccatcaaa tgctacagcc cccaggtctt ctaccccctc ccatggccaa 480 actactgcca cagageceae acetgeteag aagaeteeag ecaaagtggt gtacgtgttt 540 tctactgaga tggccaataa agctgcagaa gctgttttga agggccaggt tgaaactatc 600 gtctctttcc acatccagaa catttctaac aacaagacag agagaagcac agcgcctctg 660 aacacacaga tatctgccct tcggaatgat ccgaaacctc tcccacaaca gcccccagct 720 ccggccaacc aggaccagaa ttcttcccag aataccagac tgcagccaac tccacccatt 780 ccggcaccag cacccaagcc tgccgcaccc ccacgtcccc tggaccggga gagtcctggg 840 gtagaaaaca aactgattcc ttctgtagga agtcctgcca gctccactcc actgcccca 900 gatggtactg ggcccaactc aactcccaac aatagggcag tgacccctgt ctcccagggg 960 agcaatagct cttcagcaga tcccaaagcc cctccgcctc caccagtgtc cagtggcgag 1020 cccccacac tgggagagaa tcccgatggc ctatctcagg agcagctgga gcaccgggag. cgctccttac aaactctcag agatatccag cgcatgcttt ttcctgatga gaaagaattc 1140 acaggagcac aaagtggggg accgcagcag aatcctgggg tattagatgg gcctcagaaa 1200 aaaccagaag ggccaataca ggccatgatg gcccaatccc aaagcctagg taagggacct 1260 gggccccgga cagacgtggg agctccattt ggccctcaag gacatagaga tgtacccttt 1320 tctccagatg aaatggttcc accttctatg aactcccagt ctgggaccat aggacccgac 1380 caccttgacc atatgactcc cgagcagata gcgtggctga aactgcagca ggagttttat 1440 gaagagaaga ggaggaagca ggaacaagtg gttgtccagc agtgttccct ccaggacatg 1500

atggtccatc	agcacgggcc	tcggggagtg	gtccgaggac	cccccctcc	ataccagatg	1560
acccctagtg	aaggctgggc	acctgggggt	acagagccat	tttctgatgg	tatcaacatg	1620
ccacattctc	tgcccccgag	gggcatggct	ccccacccca	acatgccagg	gagccagatg	1680
cgcctccctg	gatttgcagg	catgataaac	tctgaaatgg	aagggccgaa	tgtccccaac	1740
cctgcatcta	gaccaggtct	ttctggagtc	agttggccag	atgatgtgcc	aaaaatccca	1800
gatggtcgaa	attttcctcc	tggccagggc	attttcagcg	gtcctggccg	aggggaacgc	1860
ttcccaaacc	cccaaggatt	gtctgaagag	atgtttcagc	agcagctggc	agagaaacag	1920
ctgggtctcc	ccccagggat	ggccatggaa	ggcatcaggc	ccagcatgga	gatgaacagg	1980
atgattccag	gctcccagcg	ccacatggag	cctgggaata	accccatttt	ccctcgaata	2040
ccagttgagg	gccctctgag	tccttctagg	ggtgactttc	caaaaggaat	tccccacag	2100
atgggccctg	gtcgggaact	tgagtttggg	atggttccta	gtgggatgaa	gggagatgtc	2160
aatctaaatg	tcaacatggg	atccaactct	cagatgatac	ctcagaagat	gagagaggct	2220
ggg gcgggcc	ctgaggagat	gctgaaatta	cgcccaggtg	gctcagacat	gctgcctgct	2280
cagcagaaga	tggtgccact	gccatttggt	gagcaccccc	agcaggagta	tggcatgggc	2340
cccagaccat	tccttcccat	gtctcagggt	ccaggcagca	acagtggctt	gcggaatctc	2400
agagaaccaa	ttgggcccga	ccagaggact	aacagccggc	tcagtcatat	gccaccacta	2460
cctctcaacc	cttccagtaa	ccccaccagc	ctcaacacag	ctcctccagt	tcagcgcggc	2520
ctggg gcgga	agcccttgga	tatatctgtg	gcaggcagcc	aggtgcattc	cccaggcatt	2580
aaccctctga	agtctcccac	gatgcaccaa	gtccagtcac	caatgctggg	ctcgccctcg	2640
gggaacctca	agtcccccca	gactccatcg	cagctggcag	gcatgctggc	gggcccagct	2700
gctgctgctt	ccattaagtc	ccccctgtt	ttggggtctg	ctgctgcttc	acctgtccac	2760
ctcaagtctc	catcacttcc	tgccccgtca	cctggatgga	cctcttctcc	aaaacctccc	2820
cttcagagtc	ctgggatccc	tccaaaccat	aaagcacccc	tcaccatggc	ctcccagcc	2880
atgctgggaa	atgtagagtc	aggtggcccc	ccacctccta	cagccagcca	gcctgcctct	2940
gtgaatatcc	ctggaagtct	tccctctagt	acaccttata	ccatgcctcc	agagccaacc	3000
ctttcccaga	acccactctc	tattatgatg	tctcgaatgt	ccaagtttgc	aatgcccagt	3060
tccaccccgt	tataccatga	tgctatcaag	actgtggcca	gctcagatga	cgactcccct	3120
ccagctcgtt	ctcccaactt	gccatcaatg	aataatatgc	caggaatggg	cattaataca	3180
cagaatcctc	gaatttcagg	tccaaacccc	gtggttccga	tgccaaccct	cagcccaatg	3240

•

ggaatgaccc agccactttc tcactccaat cagatgccct ctccaaatgc cgtgggaccc 3300 aacatacctc ctcatggggt cccaatgggg cctggcttga tgtcacacaa tcctatcatg 3360 gggcatgggt cccaggagcc accgatggta cctcaaggac ggatgggctt ccccagggc 3420 ttccctccag tacagtctcc cccacagcag gttccattcc ctcacaatgg ccccagtggg 3480 gggcagggca gcttcccagg agggatgggt ttcccaggag aaggccccct tggccgcccc 3540 agcaacctgc cccaaagttc agcagatgca gcactttgca agcctggagg ccccgggggt 3600 cctgactcct tcactgtcct ggggaacagc atgccttcgg tgtttacaga cccagatctg 3660 caggaggtca tccgacctgg agccaccgga atacctgagt ttgatctatc ccgcattatt 3720 ccatctgaga agcccagcca gacgctgcaa tatttccctc gaggggaagt tccaggccgt 3780 aaacagcccc agggtcctgg acctgggttt tcacacatgc aggggatgat gggcgaacaa 3840 gcccccagaa tgggactagc attacctggc atgggaggtc cagggccagt gggaactccg 3900 gacatccctc ttggtacagc tccatccatg ccaggccaca accccatgag accaccagcc 3960 tttctccaac aaggcatgat gggacctcac catcggatga tgtcaccagc acaatctaca 4020 atgcccggcc agcccaccct gatgagcaat ccagctgctg ccgtgggcat gattcctggc 4080 aaggatcggg ggcctgccgg gctctacacc caccctgggc ctgtgggctc tccaggcatg 4140 atgatgtcca tgcagggcat gatgggaccc caacagaaca tcatgatccc cccacagatg 4200 aggccccggg gcatggctgc tgacgtgggc atgggtggat ttagccaagg acctggcaac 4260 ccaggaaaca tgatgtttta a 4281

<210> 15

<211> 1426

<212> PRT

<213> Human lgs/bcl9

<400> 15

Met His Ser Ser Asn Pro Lys Val Arg Ser Ser Pro Ser Gly Asn Thr 1 5 10 15

Gln Ser Ser Pro Lys Ser Lys Gln Glu Val Met Val Arg Pro Pro Thr 20 25 30

Val Met Ser Pro Ser Gly Asn Pro Gln Leu Asp Ser Lys Phe Ser Asn 35 40 45

- Gln Gly Lys Gln Gly Gly Ser Ala Ser Gln Ser Gln Pro Ser Pro Cys
 50 55 60
- Asp Ser Lys Ser Gly Gly His Thr Pro Lys Ala Leu Pro Gly Pro Gly 65 70 75 80
- Gly Ser Met Gly Leu Lys Asn Gly Ala Gly Asn Gly Ala Lys Gly Lys
 85 90 95
- Gly Lys Arg Glu Arg Ser Ile Ser Ala Asp Ser Phe Asp Gln Arg Asp
 100 105 110
- Pro Gly Thr Pro Asn Asp Asp Ser Asp Ile Lys Glu Cys Asn Ser Ala 115 120 125
- Asp His Ile Lys Ser Gln Asp Ser Gln His Thr Pro His Ser Met Thr 130 135 140
- Pro Ser Asn Ala Thr Ala Pro Arg Ser Ser Thr Pro Ser His Gly Gln
 145 150 155 160
- Thr Thr Ala Thr Glu Pro Thr Pro Ala Gln Lys Thr Pro Ala Lys Val 165 170 175
- Val Tyr Val Phe Ser Thr Glu Met Ala Asn Lys Ala Ala Glu Ala Val 180 185 190
- Leu Lys Gly Gln Val Glu Thr Ile Val Ser Phe His Ile Gln Asn Ile 195 200 205
- Ser Asn Asn Lys Thr Glu Arg Ser Thr Ala Pro Leu Asn Thr Gln Ile 210 215 220
- Ser Ala Leu Arg Asn Asp Pro Lys Pro Leu Pro Gln Gln Pro Pro Ala 225 230 235 240
- Pro Ala Asn Gln Asp Gln Asn Ser Ser Gln Asn Thr Arg Leu Gln Pro 245 250 255
- Thr Pro Pro Ile Pro Ala Pro Ala Pro Lys Pro Ala Ala Pro Pro Arg 260 265 270
- Pro Leu Asp Arg Glu Ser Pro Gly Val Glu Asn Lys Leu Ile Pro Ser

Val Gly Ser Pro Ala Ser Ser Thr Pro Leu Pro Pro Asp Gly Thr Gly 290 295 300

- Pro Asn Ser Thr Pro Asn Asn Arg Ala Val Thr Pro Val Ser Gln Gly 305 310 315 320
- Ser Asn Ser Ser Ser Ala Asp Pro Lys Ala Pro Pro Pro Pro Pro Val 325 330 335
- Ser Ser Gly Glu Pro Pro Thr Leu Gly Glu Asn Pro Asp Gly Leu Ser 340 350
- Gln Glu Gln Leu Glu His Arg Glu Arg Ser Leu Gln Thr Leu Arg Asp 355 360 365
- Ile Gln Arg Met Leu Phe Pro Asp Glu Lys Glu Phe Thr Gly Ala Gln 370 380
- Ser Gly Gly Pro Gln Gln Asn Pro Gly Val Leu Asp Gly Pro Gln Lys 385 390 395 400
- Lys Pro Glu Gly Pro Ile Gln Ala Met Met Ala Gln Ser Gln Ser Leu 405 410 415
- Gly Lys Gly Pro Gly Pro Arg Thr Asp Val Gly Ala Pro Phe Gly Pro 420 425 430
- Gln Gly His Arg Asp Val Pro Phe Ser Pro Asp Glu Met Val Pro Pro 435 440 445
- Ser Met Asn Ser Gln Ser Gly Thr Ile Gly Pro Asp His Leu Asp His 450 455 460
- Met Thr Pro Glu Gln Ile Ala Trp Leu Lys Leu Gln Gln Glu Phe Tyr 465 470 475 480
- Glu Glu Lys Arg Arg Lys Gln Glu Gln Val Val Gln Gln Gln Cys Ser 485 490 495
- Leu Gln Asp Met Met Val His Gln His Gly Pro Arg Gly Val Val Arg 500 505 510

Gly Gly Thr Glu Pro Phe Ser Asp Gly Ile Asn Met Pro His Ser Leu Pro Pro Arg Gly Met Ala Pro His Pro Asn Met Pro Gly Ser Gln Met Arg Leu Pro Gly Phe Ala Gly Met Ile Asn Ser Glu Met Glu Gly Pro Asn Val Pro Asn Pro Ala Ser Arg Pro Gly Leu Ser Gly Val Ser Trp Pro Asp Asp Val Pro Lys Ile Pro Asp Gly Arg Asn Phe Pro Pro Gly Gln Gly Ile Phe Ser Gly Pro Gly Arg Gly Glu Arg Phe Pro Asn Pro Gln Gly Leu Ser Glu Glu Met Phe Gln Gln Gln Leu Ala Glu Lys Gln Leu Gly Leu Pro Pro Gly Met Ala Met Glu Gly Ile Arg Pro Ser Met Glu Met Asn Arg Met Ile Pro Gly Ser Gln Arg His Met Glu Pro Gly Asn Asn Pro Ile Phe Pro Arg Ile Pro Val Glu Gly Pro Leu Ser Pro Ser Arg Gly Asp Phe Pro Lys Gly Ile Pro Pro Gln Met Gly Pro Gly Arg Glu Leu Glu Phe Gly Met Val Pro Ser Gly Met Lys Gly Asp Val

Asn Leu Asn Val Asn Met Gly Ser Asn Ser Gln Met Ile Pro Gln Lys

Gly Pro Pro Pro Tyr Gln Met Thr Pro Ser Glu Gly Trp Ala Pro

- Met Arg Glu Ala Gly Ala Gly Pro Glu Glu Met Leu Lys Leu Arg Pro
 740 745 750
- Gly Gly Ser Asp Met Leu Pro Ala Gln Gln Lys Met Val Pro Leu Pro 755 760 765
- Phe Gly Glu His Pro Gln Gln Glu Tyr Gly Met Gly Pro Arg Pro Phe 770 780
- Leu Pro Met Ser Gln Gly Pro Gly Ser Asn Ser Gly Leu Arg Asn Leu 785 790 795 800
- Arg Glu Pro Ile Gly Pro Asp Gln Arg Thr Asn Ser Arg Leu Ser His 805 810 815
- Met Pro Pro Leu Pro Leu Asn Pro Ser Ser Asn Pro Thr Ser Leu Asn 820 825 830
- Thr Ala Pro Pro Val Gln Arg Gly Leu Gly Arg Lys Pro Leu Asp Ile 835 840 845
- Ser Val Ala Gly Ser Gln Val His Ser Pro Gly Ile Asn Pro Leu Lys 850 855 860
- Ser Pro Thr Met His Gln Val Gln Ser Pro Met Leu Gly Ser Pro Ser 865 870 875 880
- Gly Asn Leu Lys Ser Pro Gln Thr Pro Ser Gln Leu Ala Gly Met Leu 885 890 895
- Ala Gly Pro Ala Ala Ala Ala Ser Ile Lys Ser Pro Pro Val Leu Gly . 900 905 910
- Ser Ala Ala Ser Pro Val His Leu Lys Ser Pro Ser Leu Pro Ala 915 920 925
- Pro Ser Pro Gly Trp Thr Ser Ser Pro Lys Pro Pro Leu Gln Ser Pro 930 940
- Gly Ile Pro Pro Asn His Lys Ala Pro Leu Thr Met Ala Ser Pro Ala 945 950 955 960

- Met Leu Gly Asn Val Glu Ser Gly Gly Pro Pro Pro Pro Thr Ala Ser 965 970 975
- Gln Pro Ala Ser Val Asn Ile Pro Gly Ser Leu Pro Ser Ser Thr Pro 980 985 990
- Tyr Thr Met Pro Pro Glu Pro Thr Leu Ser Gln Asn Pro Leu Ser Ile 995 1000 1005
- Met Met Ser Arg Met Ser Lys Phe Ala Met Pro Ser Ser Thr Pro 1010 1015 1020
- Leu Tyr His Asp Ala Ile Lys Thr Val Ala Ser Ser Asp Asp Asp 1025 1030 1035
- Ser Pro Pro Ala Arg Ser Pro Asn Leu Pro Ser Met Asn Asn Met 1040 1050
- Pro Gly Met Gly Ile Asn Thr Gln Asn Pro Arg Ile Ser Gly Pro 1055 1060 1065
- Asn Pro Val Val Pro Met Pro Thr Leu Ser Pro Met Gly Met Thr 1070 1080
- Gln Pro Leu Ser His Ser Asn Gln Met Pro Ser Pro Asn Ala Val 1085 1090 1095
- Gly Pro Asn Ile Pro Pro His Gly Val Pro Met Gly Pro Gly Leu 1100 1105 1110
- Met Ser His Asn Pro Ile Met Gly His Gly Ser Gln Glu Pro Pro 1115 1120 1125
- Met Val Pro Gln Gly Arg Met Gly Phe Pro Gln Gly Phe Pro Pro 1130 1135 1140
- Val Gln Ser Pro Pro Gln Gln Val Pro Phe Pro His Asn Gly Pro 1145 1150 1155
- Ser Gly Gly Gln Gly Ser Phe Pro Gly Gly Met Gly Phe Pro Gly 1160 1165 1170
- Glu Gly Pro Leu Gly Arg Pro Ser Asn Leu Pro Gln Ser Ser Ala

Asp Ala Leu Cys Lys Pro Gly Gly Pro Gly Gly Pro Asp Ser Phe Thr Val Leu Gly Asn Ser Met Pro Ser Val Phe Thr Asp Pro Asp Leu Gln Glu Val Ile Arg Pro Gly Ala Thr Gly Ile Pro Glu Phe Asp Leu Ser Arg Ile Ile Pro Ser Glu Lys Pro Ser Gln Thr Leu Gln Tyr Phe Pro Arg Gly Glu Val Pro Gly Arg Lys Gln Pro Gln Gly Pro Gly Pro Ser His Met Gln Gly Met Met Gly Glu Gln Ala Pro Arg Met Gly Leu Ala Leu Pro Gly Met Gly Gly Pro Gly Pro Val Gly Thr Pro Asp Ile Pro Leu Gly Thr Ala Pro Ser Met Pro Gly His Asn Pro Met Arg Pro Pro Ala Phe Leu Gln Gln Gly Met Met Gly Pro His His Arg Met Met Ser Pro Ala Gln Ser Thr Met Pro Gly Gln Pro Thr Leu Met Ser Asn Pro Ala Ala Ala Val Gly Met Ile Pro Gly Lys Asp Arg Gly Pro Ala Gly Leu Tyr Thr His Pro Gly Pro Val Gly Ser Pro Gly Met Met Met Ser Met Gln Gly Met Met Gly Pro Gln Gln Asn Ile Met Ile Pro Pro

Gln Met Arg Pro Arg Gly Met Ala Ala Asp Val Gly Met Gly Gly 1400 1405 1410

Phe Ser Gln Gly Pro Gly Asn Pro Gly Asn Met Met Phe 1415 1420 1425

<210> 16 <211> 3948 <212> DNA

<213> Human lgs-1

<400> 16

atggcctgct	tcccatcccc	tgctgccatc	tcctgcaccc	ttagggcaca	gtgggcatct	60
cgggagctgc	tcagcggaca	gactagggtt	acccccaccc	caggaggaga	gaagctccag	120
ggagcccgcc	gctgtccccc	gcggtcattg	cccctgccc	cagccaagcc	aatgcaccca	180
gaaaataaat	tgaccaatca	tggcaagaca	gggaatggcg	gggcccaatc	tcagcaccag	240
aatgtgaacc	aaggacccac	ctgcaacgtg	ggctcgaagg	gcgtgggggc	ggggaaccat	300
ggggccaagg	ccaaccagat	ctcgcctagc	aactcaagtc	tgaagaaccc	ccaggcaggg	360
gtgccccctt	tcagctcgct	caagggcaag	gtgaagaggg	accggagtgt	gtctgtggac	420
tctggagagc	agcgagaggc	tgggacccca	tccctggatt	cagaggccaa	agaggtggcg	480
ccgcggagta	agcggcgctg	tgtgctggag	cggaagcagc	cgtacagtgg	ggacgaatgg	540
tgctctggac	cggacagtga	ggaggacgac	aagcccattg	gggccaccca	caaagctgct	600
ttcaaagaag	acggctttca	ggacaaggca	tcacacttct	tctccagcac	gtacagtcct	660
gaaacctcca	ggaggaagct	gccccaagcc	ccgaaggctt	ccttcctggg	gcagcagggc	720
cgagtcattt	ggaaacctct	ctcggaggag	ctccgtgatc	aaggtgcaga	tgcggcaggt	780
gggccggcct	caatcatgtc	tccaatcgcg	acggtgaatg	cgagtggctt	gtccaaagag	840
cagetggage	atcgggaacg	gtccctccag	acgctgcgag	acattgagcg	actgctgctc	900
cgcagcggag	agactgagcc	cttcctcaag	ggggccccca	ggaggagcgg	cgggctgaag	960
aaatatgagg	aacccttgca	gtccatgatt	tcacagacac	agagcctagg	gggccccccg	1020
ctggagcatg	aagtgcctgg	gcaccccccg	ggtggggaca	tggggcagca	gatgaacatg	1080
atgatacaga	ggctgggcca	ggacagcctc	acgcctgagc	aggtggcctg	gcgcaagctg	1140
caggaggagt	actacgaaga	gaaacggcgg	aaagaggaac	agattgggct	gcatgggagc	1200
cgtcctctgc	aggacatgat	gggcatgggg	ggcatgatgg	tgagggggcc	cccgcctcct	1260

taccacagca agcctgggga tcagtggcca cctggaatgg gtgcgcagct gcggggg	ccc 1320
atggatgttc aagatcccat gcagctccgg ggcggacctc cctttcctgg gccccgt	ttc 1380
ccaggcaacc agatacaacg ggtacctggg tttgggggca tgcagagtat gcccatg	gag 1440
gtgcccatga atgccatgca gaggcccgtg agaccaggca tgggctggac cgaagac	ttg 1500
ccccctatgg ggggacccag caattttgcc cagaacacca tgccctaccc aggtggg	cag 1560
ggtgaggcgg agcgattcat gactccccgg gtccgtgagg agctgctgcg gcaccag	ctg 1620
ctggagaage ggtcgatggg catgcagcgc cccctgggca tggcaggcag tggcatg	g ga 1680
cagagcatgg agatggagcg gatgatgcag gcgcaccgac agatggatcc tgccatg	ttt 1740
cccgggcaga tggctggtgg tgagggcctg gcgggcactc ccatgggcat ggagttt	ggt 1800
ggaggccggg gcctcctgag ccctcccatg gggcagtctg ggctgaggga ggtggac	cca 1860
cccatggggc caggcaacct caacatgaac atgaatgtca acatgaacat gaacatg	aac 1920
ctgaacgtgc agatgacccc gcagcagcag atgctgatgt cgcagaagat gcggggc	ecct 1980
ggggacttga tggggcccca gggcctcagt cctgaggaga tggcccgggt tcgggcc	cag 2040
aacagcagtg gcatggtgcc cttgccttct gccaacccgc caggacctct caagtcg	gccc 2100
caggtcctcg gctcctccct cagtgtccgt tcacccactg gctcgcccag caggctc	aag 2160
teteetteea tggeggtgee tteteeagge tgggttgeet cacceaagae ggeeatg	gccc 2220
agcccggggg tctcccagaa caagcagccg cctctcaaca tgaactcttc caccacc	ctg 2280
agcaacatgg aacaggaccc cacaccttcc cagaaccccc tgtcactgat gatgacc	cag 2340
atgtccaagt acgccatgcc cagctccacc ccgctctacc acaatgccat caagacc	atc 2400
gccacctcag acgacgaget getgcccgae cggcccctgc tgcccccccc accacca	accg 2460
cagggeteeg ggeeaggtgg eecegaetee etgaatgeee eetgtggeee agtgeee	agc _ 2520
tecteccaga tgatgeeett ecceetegg etgeageage eccatggtge catggee	ccc 2580
actgggggtg gggggggg gcctggcctg cagcagcact acccgtcagg catggcc	ctg 2640
cctcccgagg acctgcccaa ccagccgcca ggccccatgc ctccccagca gcacctg	gatg 2700
ggcaaagcca tggctgggcg catgggcgac gcatacccac cgggtgtgct ccctggg	ggtg 2760
gcatcagtgc tgaacgaccc cgagctgagc gaggtgatcc ggcccacccc aacgggg	gatc 2820
cccgagttcg acttgtcgag gatcatcccc tctgagaagc caagcagcac cctccag	gtac 2880
ttccccaaga gcgagaacca gcccccaag gctcagcccc ctaatctgca tctcatg	gaac 2940

ctgcagaaca tgatggcgga gcagactccc tctcggcctc ccaacctccc aggccagcag 3000 ggcgatcggc cgctggtggt ggtgataccg ggtacccggg ctatggcgcc ggcgcagcgc 3060 tgccctctgt gccgccagac cttcttctgt ggtcgcgggc acgtttacag ccgcaagcac 3120 cagcggcagc tgaaggaggc tttggagagg ctcctgcccc aggtggaggc ggcccgcaag 3180 gccatccgcg ccgctcaggt ggagcgctat gtgcccgaac acgagcgatg ctgctggtgc 3240 ctgtgctgcg gctgtgaggt gcgggaacac ctgagccatg gaaacctgac ggtgctgtac 3300 ggggggctgc tggagcatct ggccagccca gagcacaaga aagcaaccaa caaattctgg 3360 tgggagaaca aagctgaggt ccagatgaaa gagaagtttc tggtcactcc ccaggattat 3420 gcgcgattca agaaatccat ggtgaaaggt ttggattcct atgaagaaaa ggaggataaa 3480 gtgatcaagg agatggcagc tcagatccgt gaggtggagc agagccgaca ggaggtggtt 3540 cggtctgtct tagagacagg tcccccaaga tacgccctca cagtccggtc ccccgccgtc 3600 ctctcccggc gcacgctcaa gtccggtgcc ttccccccgc agacccccga ggcgcaccct 3660 caageteggt geetetgege eeeeggagg ggegeeetea ageetgagee eeeegggege 3720 acceteaage teggtgtace ecceeatace accegeaagg egegeeetea tgeegegaag 3780 acttcgcccc gcccaaggtg cacccgtcaa gccccgaata aaacccagtc actccaactt 3840 gcaggcaaag ctagaaaaac tgcgctgcat ttgcaaacaa aagctcttgt tggcgatgac 3900 gatactgttt tgggtgtgaa actgtcaatt gctaactacg atctgtga 3948

<210> 17

<211> 1115

<212> PRT

<213> Human lgs-1

<400> 17

Phe Lys Glu Asp Gly Phe Gln Asp Lys Ala Ser His Phe Phe Ser Ser 1 5 10 15

Thr Tyr Ser Pro Glu Thr Ser Arg Arg Lys Leu Pro Gln Ala Pro Lys 20 25 30

Ala Ser Phe Leu Gly Gln Gln Gly Arg Val Ile Trp Lys Pro Leu Ser 35 40 45

Glu Glu Leu Arg Asp Gln Gly Ala Asp Ala Ala Gly Gly Pro Ala Ser 50 55 60

Ile 65	Met	Ser	Pro	Ile	Ala 70	Thr	Val	Asn	Ala	Ser 75	Gly	Leu	Ser	Lys	Glu 80
Gln	Leu	Glu	His	Arg 85	Glu	Arg	Ser	Leu	Gln 90	Thr	Leu	Arg	Asp	Ile 95	Glu
Arg	Leu	Leu	Leu 100	Arg	Ser	Gly	Glu	Thr 105	Glu	Pro	Phe	Leu	Lys 110	Gly	Ala
Pro	Arg	Arg 115	Ser	Gly	Gly	Leu	Lys 120	Lys	Tyr	Glu	Glu	Pro 125	Leu	Gln	Ser
Met	Ile 130	Ser	Gln	Thr	Gln	Ser 135	Leu	Gly	Gly	Pro	Pro 140	Leu	Glu	His	Glu
Val 145	Pro	Gly	His	Pro	Pro 150	Gly	Gly	Asp	Met	Gly 155	Gln	Gln	Met	Asn	Met 160
Met	Ile	Gln	Arg	Leu 165	Gly	Ģln	Asp	Ser	Leu 170	Thr	Pro	Glu	Gln	Val 175	Ala
Trp	Arg	Lys	Leu 180	Gln	Glu	Glu	Tyr	Tyr 185	Glu	Glu	Lys	Arg	Arg 190	Lys	Glu
Glu	Gln	Ile 195	Gly	Leu	His	Gly	Ser 200	Arg	Pro	Leu	Gln	Asp 205	Met	Met	Gly
Met	Gly 210	Gly	Met	Met	Val	Arg 215	Gly	Pro	Pro	Pro	Pro 220	Tyr	His	Ser	Lys
Pro 225	Gly	Asp	Gln	Trp	Pro 230	Pro	Gly	Met	Gly	Ala 235		Leu	Arg	Gly	Pro 240
Met	Asp	Val	Gln	Asp 245	Pro	Met	Gln	Leu	Arg 250	Gly	Gly	Pro	Pro	Phe 255	Pro
Gly	Pro	Arg	Phe 260	Pro	Gly	Asn	Gln	Ile 265	Gln	Arg	Val	Pro	Gly 270	Phe	Gly
<i>α</i> 1		~ 3	_		_		- 3		_						

Gly Met Gln Ser Met Pro Met Glu Val Pro Met Asn Ala Met Gln Arg

	290	Arg	110	Cly	1100	295	115		Giu	ASP	300	710		rice	Cly
Gly 305	Pro	Ser	Asn	Phe	Ala 310	Gln	Asn	Thr	Met	Pro 315	Tyr	Pro	Gly	Gly	Gln 320
Gly	Glu	Ala	Glu	Arg 325	Phe	Met	Thr	Pro	Arg 330	Val	Arg	Glu	Glu	Leu 335	Leu
Arg	His	Gln	Leu 340	Leu	Glu	Lys	Arg	Ser 345	Met	Gly	Met	Gln	Arg 350	Pro	Leu
Gly	Met	Ala 355	Gly	Ser	Gly	Met	Gly 360	Gln	Ser	Met	Glu	Met 365	Glu	Arg	Met
Met	Gln 370	Ala	His	Arg	Gln	Met 375	Asp	Pro	Ala	Met	Phe 380	Pro	Gly	Gln	Met
Ala 385	Gly	Gly	Glu	Gly	Leu 390	Ala	Gly	Thr	Pro	Met 395	Gly	Met	Glu	Phe	Gly 400
Gly	Gly	Arg	Gly	Leu 405	Leu	Ser	Pro	Pro	Met 410	Gly	Gln	Ser	Gly	Leu 415	Arg
Glu	Val	Asp	Pro 420	Pro	Met	Gly	Pro	Gly 425	Asn	Leu	Asn	Met	Asn 430	Met	Asn
Val	Asn	Met 435	Asn	Met	Asn	Met	Asn 440	Leu	Asn	Val	Gln	Met 445	Thr	Pro	Gln
Gln	Gln 450	Met	Leu	Met	Ser	Gln 455	Lys	Met	Arg	Gly	Pro 460	Gly	Asp	Leu	Met
Gly 465	Pro	Gln	Gly	Leu	Ser 470	Pro	Glu	Glu	Met	Ala 475	Arg	Val	Arg	Ala	Gln 480
Asn	Ser	Ser	Gly	Met 485	Val	Pro	Leu	Pro	Ser 490	Ala	Asn	Pro	Pro	Gly 495	Pro
Leu	Lys	Ser	Pro 500	Gln	Val	Leu	Gly	Ser 505	Ser	Leu	Ser	Val	Arg 510	Ser	Pro
Thr	Gly	Ser	Pro	Ser	Arg	Leu	Lys	Ser	Pro	Ser	Met	Ala	Val	Pro	Ser

Pro Val Arg Pro Gly Met Gly Trp Thr Glu Asp Leu Pro Pro Met Gly

Pro Gly Trp Val Ala Ser Pro Lys Thr Ala Met Pro Ser Pro Gly Val 530 540

Ser Gln Asn Lys Gln Pro Pro Leu Asn Met Asn Ser Ser Thr Thr Leu 545 550 560

Ser Asn Met Glu Gln Asp Pro Thr Pro Ser Gln Asn Pro Leu Ser Leu 565 570 575

Met Met Thr Gln Met Ser Lys Tyr Ala Met Pro Ser Ser Thr Pro Leu 580 590

Tyr His Asn Ala Ile Lys Thr Ile Ala Thr Ser Asp Asp Glu Leu Leu 595 600 605

Pro Asp Arg Pro Leu Leu Pro Pro Pro Pro Pro Pro Gln Gly Ser Gly 610 620

Pro Gly Gly Pro Asp Ser Leu Asn Ala Pro Cys Gly Pro Val Pro Ser 625 630 635

Ser Ser Gln Met Met Pro Phe Pro Pro Arg Leu Gln Gln Pro His Gly 645 650 655

Ala Met Ala Pro Thr Gly Gly Gly Gly Gly Gly Pro Gly Leu Gln Gln 660 665 670

His Tyr Pro Ser Gly Met Ala Leu Pro Pro Glu Asp Leu Pro Asn Gln 675 680 685

Pro Pro Gly Pro Met Pro Pro Gln Gln His Leu Met Gly Lys Ala Met 690 695 700

Ala Gly Arg Met Gly Asp Ala Tyr Pro Pro Gly Val Leu Pro Gly Val 705 710 715 720

Ala Ser Val Leu Asn Asp Pro Glu Leu Ser Glu Val Ile Arg Pro Thr 725 730 735

Pro Thr Gly Ile Pro Glu Phe Asp Leu Ser Arg Ile Ile Pro Ser Glu
740 745 750

Lys Pro Ser Ser Thr Leu Gln Tyr Phe Pro Lys Ser Glu Asn Gln Pro
755 760 765

Pro Lys Ala Gln Pro Pro Asn Leu His Leu Met Asn Leu Gln Asn Met 770 775 780

Met Ala Glu Gln Thr Pro Ser Arg Pro Pro Asn Leu Pro Gly Gln Gln 785 790 795 800

Gly Asp Arg Pro Leu Val Val Val Ile Pro Gly Thr Arg Ala Met Ala 805 810 815

Pro Ala Gln Arg Cys Pro Leu Cys Arg Gln Thr Phe Phe Cys Gly Arg 820 825 830

Gly His Val Tyr Ser Arg Lys His Gln Arg Gln Leu Lys Glu Ala Leu 835 840 845

Glu Arg Leu Leu Pro Gln Val Glu Ala Ala Arg Lys Ala Ile Arg Ala 850 855 860

Ala Gln Val Glu Arg Tyr Val Pro Glu His Glu Arg Cys Cys Trp Cys 865 870 875 880

Leu Cys Cys Gly Cys Glu Val Arg Glu His Leu Ser His Gly Asn Leu 885 890 895

Thr Val Leu Tyr Gly Gly Leu Leu Glu His Leu Ala Ser Pro Glu His 900 905 910

Lys Lys Ala Thr Asn Lys Phe Trp Trp Glu Asn Lys Ala Glu Val Gln 915 920 925

Met Lys Glu Lys Phe Leu Val Thr Pro Gln Asp Tyr Ala Arg Phe Lys 930 935 940

Lys Ser Met Val Lys Gly Leu Asp Ser Tyr Glu Glu Lys Glu Asp Lys 945 950 955 960

Val Ile Lys Glu Met Ala Ala Gln Ile Arg Glu Val Glu Gln Ser Arg 965 970 975 Gln Glu Val Val Arg Ser Val Leu Glu Thr Gly Pro Pro Arg Tyr Ala 980 985 990

Leu Thr Val Arg Ser Pro Ala Val Leu Ser Arg Arg Thr Leu Lys Ser 995 1000 1005

Gly Ala Phe Pro Pro Gln Thr Pro Glu Ala His Pro Gln Ala Arg 1010 1015 1020

Cys Leu Cys Ala Pro Arg Arg Gly Ala Leu Lys Pro Glu Pro Pro 1025 1030 1035

Gly Arg Thr Leu Lys Leu Gly Val Pro Pro His Thr Thr Arg Lys
1040 1050

Ala Arg Pro His Ala Ala Lys Thr Ser Pro Arg Pro Arg Cys Thr 1055 1065

Arg Gln Ala Pro Asn Lys Thr Gln Ser Leu Gln Leu Ala Gly Lys 1070 1075 1080

Ala Arg Lys Thr Ala Leu His Leu Gln Thr Lys Ala Leu Val Gly 1085 1090 1095

Asp Asp Asp Thr Val Leu Gly Val Lys Leu Ser Ile Ala Asn Tyr 1100 1105 1110

Asp Leu 1115

<210> 18 <211> 49

<212> DNA

<213> Artificial

<220>

<221> misc_structure

<222> (1)..(49)

<223> T7 Promoter containing dsRNA-lgs-R1

<400> 18

taatacgact cactataggg agaccacttc catgctcatt tcgtcatta

```
<211> 48
<212> DNA
<213> Artificial
<220>
<221> misc_structure
<222> (1)..(48)
<223> dsRNA-lgs-F1
<400> 19
taatacgact cactataggg agaccactag gatctctcga caacaatg
                                                                    48
<210> 20
<211> 49
<212> DNA
<213> Artificial
<220>
<221> misc_structure
<222> (1)..(49)
<223> F Primer
<400> 20
taatacgact cactataggg agaccacaca agaccaagtg gacgatatg
                                                                    49
<210> 21
<211> 48
<212> DNA
<213> Artificial
<220>
<221> misc_structure
<222> (1)..(48)
<223> R Primer
<400> 21
taatacgact cactataggg agaccacaat ttgcaagcaa tctgtgac
                                                                    48
<210> 22
<211> 27
<212> DNA
<213> Artificial
<220>
<221> misc_structure
<222> (1)..(27)
<223> T7 Promoter
<400> 22
taatacgact cactataggg agaccac
                                                                    27
```